domain (e.g., comprising residues 114-139 of SEQ ID NO:2 or 4), a serine/threonine/proline-rich domain (e.g., comprising residues 137-168 of SEQ ID NO:2 or 4), a TRADE-related death effector domain (e.g., comprising residues 218-417 of SEQ ID NO:2 or 218-423 of SEQ ID NO:4), an N-glycosylation site (e.g., comprising residues 105-108 of SEQ ID NO:2 or 4), a cAMP/cGMP-dependent protein kinase phosphorylation site (e.g., comprising residues 200 to 203 of SEQ ID NO:2 or 4), a cAMP/cGMP-dependent protein kinase phosphorylation site (e.g., comprising residues 238 to 241 of SEQ ID NO:2 or 4), at least one protein kinase C phosphorylation site (e.g., comprising residues 205 to 207 of SEQ ID NO:2 or 4), a first casein kinase II phosphorylation site (e.g., comprising residues 219 to 222 of SEQ ID NO:2 or 4), a second casein kinase II phosphorylation site (e.g., comprising residues 325 to 328 of SEQ ID NO:2 or 4), a tyrosine kinase phosphorylation site (e.g., comprising residues 207-213 of SEQ ID NO:2 or 4), an N-myristoylation site (e.g., comprising residues 215-220 of SEQ ID NO:2 or 4), a TRAF binding domain (e.g. comprising residues 1-328 of SEQ ID NO:2 or 4, preferably comprising residues 218-328), a kinase associating domain (e.g. comprising residues 1-368 of SEQ ID NO:2 or 4, preferably comprising residues 328-368), or an NFkB activation signaling domain (e.g. comprising residues comprising residues 1-368 of SEQ ID NO:2 or 4, preferably in the intracellular domain of TRADE). TRADE molecules also lack a TNF receptor death domain consensus sequence in the intracellular portion of the TRADE peptide. The TNF receptor death domain consensus sequence, as defined for HMM searches, is illustrated by the consensus sequence listed under the PFAM Accession Number PF00531 ~~(http://pfam.wustl.edu)~~.

Replace the first partial paragraph on page 46 with the following:

215:403. BLAST nucleotide searches can be performed with the NBLAST program score=100, wordlength=12 to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score=50, wordlength=3 to obtain amino acid sequences homologous to the protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., 1997, Nucleic Acids Research 25(17):3389. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. ~~See http://www.ncbi.nlm.nih.gov~~. Another preferred, non-limiting algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, CABIOS (1989). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM 120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

Replace the second complete paragraph on page 47 with the following:

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul et al., 1990, J. Mol. Biol. 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score=100, wordlength=12 to obtain nucleotide sequences homologous to TRADE nucleic acid molecules of the invention.

BLAST protein searches can be performed with the XBLAST program, score=50, wordlength=3 to obtain amino acid sequences homologous to TRADE protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., 1997, Nucleic Acids Res. 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. For example, the nucleotide sequences of the invention can be analyzed using the default BLASTN matrix 1-3 with gap penalties set at: existence 11 and extension 1. The amino acid sequences of the invention can be analyzed using the default settings: the Blosum62 matrix with gap penalties set at existence 11 and extension 1. ~~See http://www.ncbi.nlm.nih.gov.~~

Replace the second full paragraph on page 50 with the following:

In another embodiment, a spacer of glycine and serine residues may be incorporated between the TRADE and Fc sequences. For example, a TRADE portion of a TRADE fusion protein might ordinarily terminate with the C-terminal sequence of the TRADE extracellular region: STASSPRDT (SEQ ID NO:9); or at other residues between the second cysteine-rich domain and the transmembrane and the residues of the Igγ1 hinge could be DKTHTCP (SEQ ID NO:17) (e.g., starting at residue 104 of the polypeptide sequence under accession number P01857 in the SwissProt database~~, http://www.expasy.ch/sprot~~). These could be followed by the C_H2-C_H3 domain residues or a spacer of glycine and serine residues may be incorporated between the TRADE and Fc sequences.